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RAW SEQUENCE LISTING

DATE: 09/23/2002

PATENT APPLICATION: US/10/043,539A

TIME: 10:23:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\09232002\J043539A.raw

3 <110> APPLICANT: Cheung, Ambrose
 4 Manna, Adar
 5 Zhang, Gongyi
 7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE
 DETERMINANTS IN BACTERIA

9 <130> FILE REFERENCE: DC-0199
 11 <140> CURRENT APPLICATION NUMBER: US 10/043,539A

C--> 12 <141> CURRENT FILING DATE: 2000-01-11

14 <150> PRIOR APPLICATION NUMBER: US 60/261,233

15 <151> PRIOR FILING DATE: 2001-01-12

17 <150> PRIOR APPLICATION NUMBER: US 60/261,607

18 <151> PRIOR FILING DATE: 2001-01-12

20 <150> PRIOR APPLICATION NUMBER: US 60/289,601

21 <151> PRIOR FILING DATE: 2001-05-08

23 <160> NUMBER OF SEQ ID NOS: 35

25 <170> SOFTWARE: PatentIn version 3.1

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 947

29 <212> TYPE: DNA

30 <213> ORGANISM: Staphylococcus aureus

32 <220> FEATURE:

33 <221> NAME/KEY: CDS

34 <222> LOCATION: (208)..(552)

35 <223> OTHER INFORMATION:

38 <400> SEQUENCE: 1

39 gttttcaaaa tcggtggagg tgcatgaaaa agttattggg cattttttga aaataaaaaa 60
 41 atatcaataa gttggagtca ttaccgaatt tttatactta tttgtttaga atgaacttta 120
 43 taacatagtt g gatagagtt ttcgatttaa tacattaaat gtgaaccttg ctacaacaag 180
 45 atgtgcatca gaaggagtggt ttttaata atg agt aaa att aat gat att aat gat 234
 46 Met Ser Lys Ile Asn Asp Ile Asn Asp
 47 1 5
 49 tta gtc aac gca aca ttt caa gtt aag aag ttt ttc aga gat aca aaa 282
 50 Leu Val Asn Ala Thr Phe Gln Val Lys Lys Phe Phe Arg Asp Thr Lys
 51 10 15 20 25
 53 aag aag ttc aat ttg aac tat gaa gaa att tat att tta aat cat att 330
 54 Lys Lys Phe Asn Leu Asn Tyr Glu Glu Ile Tyr Ile Leu Asn His Ile
 55 30 35 40
 57 tta aga agt gag tct aac gaa atc tca tct aaa gag att gct aag tgc 378
 58 Leu Arg Ser Glu Ser Asn Glu Ile Ser Ser Lys Glu Ile Ala Lys Cys
 59 45 50 55
 61 tca gag ttc aaa cct tac tat tta act aaa gct tta caa aag cta aaa 426
 62 Ser Glu Phe Lys Pro Tyr Tyr Leu Thr Lys Ala Leu Gln Lys Leu Lys
 63 60 65 70
 65 gat tta aaa ttg tta tca aag aaa aga agt tta caa gac gaa aga aca 474

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```

66 Asp Leu Lys Leu Leu Ser Lys Lys Arg Ser Leu Gln Asp Glu Arg Thr
67      75      80      85
69 gtt att gtt tat gtt aca gat aca caa aaa gca aat att caa aaa ctg      522
70 Val Ile Val Tyr Val Thr Asp Thr Gln Lys Ala Asn Ile Gln Lys Leu
71 90      95      100      105
73 att tca gaa tta gaa gaa tac att aaa aat taaatcaagg ttaattgcgt      572
74 Ile Ser Glu Leu Glu Glu Tyr Ile Lys Asn
75      110      115
77 ttaataacat tgaacgataa caattttatta atacgaagtt atttattcag cattggggaca      632
79 taaaattaac ttaaaatttta aatattgaag atgctttaat taaagttaaa gaccagccat      692
81 accttatttc agcttatttaa gcttgacaca aggtacacta gtctttttat tttaatattt      752
83 tcttagaaaa tcaagtttac gatcataaat attttctgcg atatagcttt ggatgggttc      812
85 aagtattttc tctataattt gtgtgcgata agcaaaaatt ctaactgcaa aaccatgtgt      872
87 aggcaattga gaaatagcaa caccacaatc ggatgtattg ctataagaac taatgggttc      932
89 ataaactgaa tcgat      947
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 115
94 <212> TYPE: PRT
95 <213> ORGANISM: Staphylococcus aureus
97 <400> SEQUENCE: 2
99 Met Ser Lys Ile Asn Asp Ile Asn Asp Leu Val Asn Ala Thr Phe Gln
100 1      5      10      15
103 Val Lys Lys Phe Phe Arg Asp Thr Lys Lys Lys Phe Asn Leu Asn Tyr
104      20      25      30
107 Glu Glu Ile Tyr Ile Leu Asn His Ile Leu Arg Ser Glu Ser Asn Glu
108      35      40      45
111 Ile Ser Ser Lys Glu Ile Ala Lys Cys Ser Glu Phe Lys Pro Tyr Tyr
112      50      55      60
115 Leu Thr Lys Ala Leu Gln Lys Leu Lys Asp Leu Lys Leu Leu Ser Lys
116 65      70      75      80
119 Lys Arg Ser Leu Gln Asp Glu Arg Thr Val Ile Val Tyr Val Thr Asp
120      85      90      95
123 Thr Gln Lys Ala Asn Ile Gln Lys Leu Ile Ser Glu Leu Glu Glu Tyr
124      100      105      110
127 Ile Lys Asn
128      115
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 124
133 <212> TYPE: PRT
134 <213> ORGANISM: Staphylococcus aureus
136 <400> SEQUENCE: 3
138 Met Ala Ile Thr Lys Ile Asn Asp Cys Phe Glu Leu Leu Ser Met Val
139 1      5      10      15
142 Thr Tyr Ala Asp Lys Leu Lys Ser Leu Ile Lys Lys Glu Phe Ser Ile
143      20      25      30
146 Ser Phe Glu Glu Phe Ala Val Leu Thr Tyr Ile Ser Glu Asn Lys Glu
147      35      40      45
150 Lys Glu Tyr Tyr Leu Lys Asp Ile Ile Asn His Leu Asn Tyr Lys Gln
151      50      55      60

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```

154 Pro Gln Val Val Lys Ala Val Lys Ile Leu Ser Gln Glu Asp Tyr Phe
155 65              70              75              80
158 Asp Lys Lys Arg Asn Glu His Asp Glu Arg Thr Val Leu Ile Leu Val
159              85              90              95
162 Asn Ala Gln Gln Arg Lys Lys Ile Glu Ser Leu Leu Ser Arg Val Asn
163              100             105             110
166 Lys Arg Ile Thr Glu Ala Asn Asn Glu Ile Glu Leu
167              115             120
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 30
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Degenerate oligonucleotide.
178 <400> SEQUENCE: 4
179 atgwsaaaaa tyaa ygatat yaaygatttt                      30
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 30
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Degenerate oligonucleotide.
190 <400> SEQUENCE: 5
191 attwsytcw swwckyaara trtgrttyaa                      30
194 <210> SEQ ID NO: 6
195 <211> LENGTH: 24
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Synthetic oligonucleotide.
202 <400> SEQUENCE: 6
203 gcatgaaaaa gatatcgggc attt                      24
206 <210> SEQ ID NO: 7
207 <211> LENGTH: 26
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Synthetic oligonucleotide.
214 <400> SEQUENCE: 7
215 gtgagtctaa cgatatctca tctaaa                      26
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 14
220 <212> TYPE: PRT
221 <213> ORGANISM: Staphylococcus aureus
223 <220> FEATURE:
224 <221> NAME/KEY: MISC_FEATURE
225 <222> LOCATION: (1)..(1)
226 <223> OTHER INFORMATION: "X" is defined as any amino acid residue.
229 <220> FEATURE:

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Input Set : A:\EP.txt

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230 <221> NAME/KEY: MISC_FEATURE
 231 <222> LOCATION: (13)..(13)
 232 <223> OTHER INFORMATION: "X" is defined as being either S or T.
 235 <400> SEQUENCE: 8
 237 Xaa Lys Ile Asn Asp Ile Asn Asp Leu Val Asn Ala Xaa Phe
 238 1 5 10
 241 <210> SEQ ID NO: 9
 242 <211> LENGTH: 8
 243 <212> TYPE: DNA
 244 <213> ORGANISM: Staphylococcus aureus
 246 <400> SEQUENCE: 9
 247 aggagtgg 8
 250 <210> SEQ ID NO: 10
 251 <211> LENGTH: 6
 252 <212> TYPE: DNA
 253 <213> ORGANISM: Staphylococcus aureus
 255 <400> SEQUENCE: 10
 256 tagaat 6
 259 <210> SEQ ID NO: 11
 260 <211> LENGTH: 6
 261 <212> TYPE: DNA
 262 <213> ORGANISM: Staphylococcus aureus
 264 <400> SEQUENCE: 11
 265 ttaccg 6
 268 <210> SEQ ID NO: 12
 269 <211> LENGTH: 20
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Staphylococcus aureus
 273 <400> SEQUENCE: 12
 274 ttactaaatt aaaaaaatta 20
 277 <210> SEQ ID NO: 13
 278 <211> LENGTH: 28
 279 <212> TYPE: DNA
 280 <213> ORGANISM: Staphylococcus aureus
 282 <400> SEQUENCE: 13
 283 taaattaatg ttatttttta ataattta 28
 286 <210> SEQ ID NO: 14
 287 <211> LENGTH: 8
 288 <212> TYPE: DNA
 289 <213> ORGANISM: Staphylococcus aureus
 291 <400> SEQUENCE: 14
 292 taaattaa 8
 295 <210> SEQ ID NO: 15
 296 <211> LENGTH: 8
 297 <212> TYPE: DNA
 298 <213> ORGANISM: Staphylococcus aureus
 300 <400> SEQUENCE: 15
 301 ataattta 8
 304 <210> SEQ ID NO: 16

RAW SEQUENCE LISTING

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```

305 <211> LENGTH: 8
306 <212> TYPE: DNA
307 <213> ORGANISM: Staphylococcus aureus
309 <400> SEQUENCE: 16
310 taaattat 8
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 20
315 <212> TYPE: DNA
316 <213> ORGANISM: Staphylococcus aureus
318 <400> SEQUENCE: 17
319 ttactaaatt aaaaaaatta 20
322 <210> SEQ ID NO: 18
323 <211> LENGTH: 49
324 <212> TYPE: DNA
325 <213> ORGANISM: Staphylococcus aureus
327 <400> SEQUENCE: 18
328 tcttaagacc taaattaatg ttatttttta ataatttaca ccaaattaa 49
331 <210> SEQ ID NO: 19
332 <211> LENGTH: 210
333 <212> TYPE: DNA
334 <213> ORGANISM: Staphylococcus aureus
336 <400> SEQUENCE: 19
337 gttttcaaaa tcggtggagg tgcattgaaaa agttattggg cattttttga aaataaaaaa 60
339 atatcaataa gttggagtca ttaccgaatt tttatactta tttgtttaga atgaacttta 120
341 taacatagtt ggatagagtt ttcgatttaa tacattaaat gtgaaccttg ctacaacaag 180
343 atgtgcatca gaaggagtgg ttttaataatg 210
346 <210> SEQ ID NO: 20
347 <211> LENGTH: 29
348 <212> TYPE: DNA
349 <213> ORGANISM: Staphylococcus aureus
351 <400> SEQUENCE: 20
352 ctaaaattaat gttatttttt aataattta 29
355 <210> SEQ ID NO: 21
356 <211> LENGTH: 3
357 <212> TYPE: DNA
358 <213> ORGANISM: Staphylococcus aureus
360 <400> SEQUENCE: 21
361 aaa 3
364 <210> SEQ ID NO: 22
365 <211> LENGTH: 20
366 <212> TYPE: DNA
367 <213> ORGANISM: Staphylococcus aureus
369 <400> SEQUENCE: 22
370 aattaccttg tattgtcgat 20
373 <210> SEQ ID NO: 23
374 <211> LENGTH: 22
375 <212> TYPE: DNA
376 <213> ORGANISM: Staphylococcus aureus
378 <400> SEQUENCE: 23

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/043,539A

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Input Set : A:\EP.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 1,13

Seq#:26; Xaa Pos. 2,4,10,15,16,17,19,20,24,25,31,38,44,45,47,51,52,58,59,61

Seq#:26; Xaa Pos. 73,77,78,86,87,95,97,99,102,106,110,114,117,118,120

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7